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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/107,979**

DATE: 07/09/98  
TIME: 13:51:02

*INPUT SET: S27313.raw*

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: Unassigned

091079 053099 860E90" 64620T60

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

(ii) TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor

(iii) NUMBER OF SEQUENCES: 23

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Genentech, Inc.
- (B) STREET: 1 DNA Way
- (C) CITY: South San Francisco
- (D) STATE: California
- (E) COUNTRY: USA
- (F) ZIP: 94080

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: Unassigned
- (B) FILING DATE: 30-Jun-1998
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Conley, Deirdre L.
- (B) REGISTRATION NUMBER: 36,487
- (C) REFERENCE/DOCKET NUMBER: P1084R1-2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 650/225-2066
- (B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2538 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mouse NRG3 nucleic acid
- (B) LOCATION: 1-2538
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGACCGGC CGGCGGCGCC CGGGCCGGTC TCGCCCCTCT ACCGAGCGCC 50  
TCGCCGCCCC CTCCCCGGCC CGCGTCCCCT CCCCCGTCCT CTCCTCCCCG 100  
CCCGCCGCCC GCCTCTCGGG GGGAGGGGCG TGGGGGCAGG GAGCCGATTT 150  
GCATGCGGCC GCCGCGGCCG CTGCCTGAGC CGGAGCCCGC CGCCGCCGGA 200  
GCCCCGCGCC GCGCCCGCGC CCGGCCCGCG CGGCCCCATG CCTCTGGCGC 250  
GGCCCTCGGG GGGGCGAAGG TGAAGATCGG CTCCTAGGAT GAGTGAAGGG 300  
GCGGCCGGTG CCTCGCCACC TGGTGCCGCT TCGGCAGCCG CCGCCTCAGC 350  
CGAGGAGGGC ACCGCGGCGG CTGCGGCGGC GGCGGCGGCG GGCGGGGGCC 400  
CGGACGGCGG CGGAGAAGGG GCGGCCGAAC CCCCCGGGA GTTACGCTGT 450  
AGCGACTGCA TCGTGTGGAA CCGGCAGCAG ACGTGGTTGT GCGTGGTGCC 500  
TCTGTTTCATC GGCTTCATCG GCCTGGGGCT CAGCCTCATG CTGCTTAAAT 550  
GGATCGTGTT AGGCTCCGTC AAGGAGTACG TGCCACGGA CCTGGTGGAC 600  
TCCAAGGGAA TGGGCCAGGA CCCCTTCTTC CTCTCCAAGC CCAGCTCTTT 650  
CCCCAAGGCT ATGGAAACCA CCACAACAAC CACTTCTACC ACGTCCCCCG 700  
CCACCCCTC TGCCGGCGGC GCCGCTTCTT CCAGGACGCC TAACCGGATT 750  
AGCACCCGCT TGACCACCAT CACACGGGCA CCCACCCGCT TCCCTGGGCA 800  
CCGGGTTCCC ATCCGGGCTA GCCCGCGCTC TACCACAGCA CGGAACACTG 850  
CTGCCCCTCC GACGGTCCTG TCCACCACGG CCCCTTTCTT CAGTAGCAGC 900  
ACGCCC GGCT CCCGACCCCC GATGCCAGGA GCCCCAGTA CGCAGGCGAT 950  
GCCTTCCTGG CCCACTGCGG CGTATGCTAC CTCCTCCTAC CTCCACGATT 1000  
CCACTCCCTC CTGGACCCTG TCACCCTTTC AGGATGCTGC TGCCGCCTCT 1050  
TCCTCCTCAC CCTCTTCAC CTCCTCCACT ACCACCACCC CAGAAACTAG 1100  
CACCAGCCCC AAATTTTATA CTACAACATA CTCCACTGAA CGATCTGAGC 1150  
ACTTCAAACC CTGTCGAGAC AAGGACCTGG CGTATTGTCT CAATGATGGT 1200

GAATGCTTTG TGATTGAGAC CCTGACAGGA TCCCATAAGC ACTGTCGGTG 1250  
 CAAGGAAGGC TACCAAGGAG TCCGTTGTGA TCAATTTCTG CCGAAAACAG 1300  
 ACTCCATCTT ATCGGATCCA ACAGACCACT TGGGGATTGA ATTCATGGAG 1350  
 AGTGAAGACG TTTATCAAAG GCAGGTGCTG TCAATTCAT GTATCATCTT 1400  
 TGGAATTGTC ATCGTGGGCA TGTTCTGTGC AGCATTCTAC TTCAAAAGCA 1450  
 AGAAACAAGC TAAACAAATT CAGGAGCACC TGAAAGAGTC ACAGAATGGG 1500  
 AAGAACTACA GCCTCAAGGC ATCCAGCACA AAGTCTGAGA GCTTGATGAA 1550  
 GAGCCATGTC CATCTACAAA ATTATTCAAA GGCGGATAGG CATCCTGTGA 1600  
 CTGCGCTGGA GAAATAATG GAGTCAAGTT TTTCAGCTCC CCAGTCGTTC 1650  
 CCAGAAGTCA CTTCTCCTGA CCGAGGAAGC CAGCCTATCA AGCACCACAG 1700  
 CCCAGGACAA AGGAGTGGGA TGTTGCATAG GAATACTTTC AGAAGGGCAC 1750  
 CACCCTCACC CCGAAGTCGA CTGGGTGGTA TTGTAGGACC AGCATATCAA 1800  
 CAACTTGAAG AATCAAGAA TCCAGACCAG GATACGATAC CTTGCCAAGG 1850  
 GATAGAGGTC AGGAAGACTA TATCCACCT GCCTATACAG CTGTGGTGTG 1900  
 TTGAAAGACC CCTGGACTTA AAGTATGTGT CCAATGGCTT AAGAACCCTA 1950  
 CAAAATGCAT CAATAAATAT GCAACTGCCT TCAAGAGAGA CAAACCCTA 2000  
 TTTTAATAGC TTGGATCAAA AGGACCTGGT GGGTTATTTA TCCCCAAGGG 2050  
 CCAATTCTGT GCCATCATC CCGTCGATGG GTCTAGAAGA AACCTGCATG 2100  
 CAAATGCCAG GGATTTCTGA CGTCAAAAGC ATTAAATGGT GCAAAAACCTC 2150  
 CTACTCCGCT GACATTGTCA ACGCGAGTAT GCCAGTCAGT GATTGTCTTC 2200  
 TAGAAGAACA ACAGGAAGTG AAAATATTAC TAGAGACTGT GCAGGAACAG 2250  
 ATCCGGATTC TGAATGATGC CAGACGGTCA GAAGACTTCG AACTGGCCAG 2300  
 CATGGAAACT GAGGACAGTG CGAGCGAAAA CACAGCCTTT CTCCCCCTGA 2350  
 GTCCCACGGC CAAATCAGAA CGAGAGGCAC AATTTGTCTT AAGAAATGAA 2400  
 ATACAAAGAG ACTCTGTGCT AACCAAGTGA CTGGAAATGT AGGAATCTGT 2450  
 GCATTATATG CTTTGCTAAA CAGGAAGGAG AGGAAATTAA ATACAAATTA 2500

TTTATATGCA TTAATTTAAG AGCATCTACT TAGAAGCC 2538

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
- (B) LOCATION: 1-713
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Glu	Gly	Ala	Ala	Gly	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	
1				5				10						15	
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	
				20				25						30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35				40						45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50				55						60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65				70						75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80				85						90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95				100						105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110				115						120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125				130						135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140				145						150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155				160						165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170				175						180	

Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Pro	Thr	Val	Leu	Ser
				185					190					195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Pro	Gly	Ser	Arg	Pro
				200					205					210
Pro	Met	Pro	Gly	Ala	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro
				215					220					225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro
				230					235					240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ala	Ala	Ser	Ser
				245					250					255
Ser	Ser	Pro	Ser	Ser	Thr	Ser	Ser	Thr	Thr	Thr	Thr	Pro	Glu	Thr
				260					265					270
Ser	Thr	Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg
				275					280					285
Ser	Glu	His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys
				290					295					300
Leu	Asn	Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser
				305					310					315
His	Lys	His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys
				320					325					330
Asp	Gln	Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr
				335					340					345
Asp	His	Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Asp	Val	Tyr	Gln
				350					355					360
Arg	Gln	Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile
				365					370					375
Val	Gly	Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln
				380					385					390
Ala	Lys	Gln	Ile	Gln	Glu	His	Leu	Lys	Glu	Ser	Gln	Asn	Gly	Lys
				395					400					405
Asn	Tyr	Ser	Leu	Lys	Ala	Ser	Ser	Thr	Lys	Ser	Glu	Ser	Leu	Met
				410					415					420
Lys	Ser	His	Val	His	Leu	Gln	Asn	Tyr	Ser	Lys	Ala	Asp	Arg	His
				425					430					435

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Ala Lys Ser Glu Arg Glu Ala Gln Phe Val Leu Arg Asn Glu Ile  
695 700 705

Gln Arg Asp Ser Val Leu Thr Lys  
710 713

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: mNRG3 extracellular domainAmino acid seq
- (B) LOCATION: 1-362
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Glu	Gly	Ala	Ala	Gly	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150	

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
- (B) LOCATION: 1-47
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn  
1 5 10 15  
Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys  
20 25 30  
His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln  
35 40 45  
Phe Leu  
47

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq.
- (B) LOCATION: 1-2502
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCACCGACCT AGTGGACTCC ACTAGGTCGG TGGGCACGTA CTCCTTGACG 50  
GAGCCACCA CGATCCATTT GAGAAGCATG AGGCGCGGCC CCATGCCTCT 100  
GCCGCGGCC TCGGGGGGGC GAAGGTGAAN ACCGGCTCCT AGGATGAGTG 150  
AAGGGGCGGC CGCTGCCTCG CCACCTGGTG CCGCTTCGGC AGCCGCCGCC 200

TCGGCCGAGG AGGGCACCGC GCGGGCTGCG GCGGCGGCAG CGGCGGGCGG 250  
 GGGCCCGGAC GCGGCGGGCG AAGGGGCGGC CGAGCCCCCC CGGGAGTTAC 300  
 GCTGTAGCGA CTGCATCGTG TGGAAACGGC AGCAGACGTG GCTGTGCGTG 350  
 GTACCTCTGT TCATCGGCTT CATCGGCCTG GGGCTCAGCC TCATGCTTCT 400  
 CAAATGGATC GTGGTGGGCT CCGTCAAGGA GTACGTGCCC ACCGACCTAG 450  
 TGGACTCCAA GGGGATGGGC CAGGACCCCT TCTTCCTCTC CAAGCCCAGC 500  
 TCTTTCCCCA AGGCCATGGA GACCACCACC ACTACCACTT CCACCACGTC 550  
 CCCC GCCACC CCCTCCGCCG GGGGTGCCGC CTCCTCCAGG ACGCCCAACC 600  
 GGATTAGCAC TCGCCTGACC ACCATCACGC GGGCGCCCAC TCGCTTCCCC 650  
 GGGCACCGGG TGCCCATCCG GGCCAGCCCG CGCTCCACCA CAGCACGGAA 700  
 CACTGCGGCC CCTGCGACGG TCCCGTCCAC CACGGCCCCG TTCTTCAGTA 750  
 GCAGCACGCT GGGCTCCCGA CCCCCGGTGC CAGGAACTCC AAGTACCCAG 800  
 GCAATGCCCT CCTGGCCTAC TGCGGCATAC GCTACCTCCT CCTACCTTCA 850  
 CGATTCTACT CCCTCCTGGA CCCTGTCTCC CTTTCAGGAT GCTGCCTCCT 900  
 CTTCTTCCTC TTCTTCCTCC TCCGCTACCA CCACCACACC AGAAACTAGC 950  
 ACCAGCCCCA AATTTTCATAC GACGACATAT TCCACAGAGC GATCCGAGCA 1000  
 CTTCAAACCC TGCCGAGACA AGGACCTTGC ATACTGTCTC AATGATGGCG 1050  
 AGTGCTTTGT GATCGAAACC CTGACCGGAT CCCATAAACA CTGTGCGGTGC 1100  
 AAAGAAGGCT ACCAAGGAGT CCGTTGTGAT CAATTTCTGC CGAAAACTGA 1150  
 TTCCATCTTA TCGGATCCAA CAGACCACTT GGGGATTGAA TTCATGGAGA 1200  
 GTGAAGAAGT TTATCAAAGG CAGGTGCTGT CAATTTTCATG TATCATCTTT 1250  
 GGAATTGTCA TCGTGGGCAT GTTCTGTGCA GCATTCTACT TCAAAAGCAA 1300  
 GAAACAAGCT AAACAAATCC AAGAGCAGCT GAAAGTGCCA CAAAATGGTA 1350  
 AAAGCTACAG TCTCAAAGCA TCCAGCACAA TGGCAAAGTC AGAGAACTTG 1400  
 GTGAAGAGCC ATGTCCAGCT GCAAAATTAT TCAAAGGTGG AAAGGCATCC 1450  
 TGTGACTGCA TTGGAGAAAA TGATGGAGTC AAGTTTTGTC GGCCCCCAGT 1500

CATTCCCTGA GGTCCCTTCT CCTGACAGAG GAAGCCAGTC TGTCAAACAC 1550  
CACAGGAGTC TATCCTCTTG CTGCAGCCCA GGGCAAAGAA GTGGCATGCT 1600  
CCATAGGAAT GCCTTCAGAA GGACACCCCC GTCACCCCGA AGTAGGCTAG 1650  
GTGGAATTGT GGGACCAGCA TATCAGCAAC TCGAAGAATC AAGGATCCCA 1700  
GACCAGGATA CGATACCTTG CCAAGGGATA GAGGTCAGGA AGACTATATC 1750  
CCACCTGCCT ATACAGCTGT GGTGTGTTGA AAGACCCCTG GACTTAAAGT 1800  
ATTCATCCAG TGGTTTAAAA ACCCAACGAA ATACATCAAT AAATATGCAA 1850  
CTGCCTTCAA GAGAGACAAA CCCCTATTTT AATAGCTTGG AGCAAAAGGA 1900  
CCTGGTGGGC TATTCATCCA CAAGGGCCAG TTCTGTGCCC ATCATCCCTT 1950  
CAGTGGGTTT AGAGGAAACC TGCCTGCAAA TGCCAGGGAT TTCTGAAGTC 2000  
AAAAGCATCA AATGGTGCAA AAACCTCTAT TCAGCTGACG TTGTCAATGT 2050  
GAGTATTCCA GTCAGCGATT GTCTTATAGC AGAACAACAA GAAGTGAAAA 2100  
TATTGCTAGA AACTGTCCAG GAGCAGATCC GAATTCTGAC TGATGCCAGA 2150  
CGGTCAGAAG ACTACGAACT GGCCAGCGTA GAAACCGAGG ACAGTGCAAG 2200  
CGAAAACACA GCCTTTCTCC CCCTGAGTCC CACAGCCAAA TCAGAACGAG 2250  
AGGCGCAATT TGTCTTAAGA AATGAAATAC AAAGAGACTC TGCATTGACC 2300  
AAGTGACTION AGATGTAGGA ATCTGTGCAT TCTATGCTTT GCTCAACAGG 2350  
AAAGAGAGGA AATCAAATAC AAATTATTTA TATGCATTAA TTTAAGAGCA 2400  
TCTACTTAGA AGAAACCAAA TAGTCTATCG CCCTCATATC ATAGTGTTTT 2450  
TTAACAAAAT ATTTTTTTAA GGGAAAGAAA TGTTTCAGGA GGGATAAAGC 2500  
TT 2502

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 amino acid sequence
- (B) LOCATION: 1-720

(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	1	5	10	15
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180	
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	185	190	195	
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	200	205	210	
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225	
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240	

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Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	
				245					250					255	
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr	
				260					265					270	
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu	
				275					280					285	
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn	
				290					295					300	
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys	
				305					310					315	
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln	
				320					325					330	
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His	
				335					340					345	
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln	
				350					355					360	
Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	Val	Gly	
				365					370					375	
Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	Ala	Lys	
				380					385					390	
Gln	Ile	Gln	Glu	Gln	Leu	Lys	Val	Pro	Gln	Asn	Gly	Lys	Ser	Tyr	
				395					400					405	
Ser	Leu	Lys	Ala	Ser	Ser	Thr	Met	Ala	Lys	Ser	Glu	Asn	Leu	Val	
				410					415					420	
Lys	Ser	His	Val	Gln	Leu	Gln	Asn	Tyr	Ser	Lys	Val	Glu	Arg	His	
				425					430					435	
Pro	Val	Thr	Ala	Leu	Glu	Lys	Met	Met	Glu	Ser	Ser	Phe	Val	Gly	
				440					445					450	
Pro	Gln	Ser	Phe	Pro	Glu	Val	Pro	Ser	Pro	Asp	Arg	Gly	Ser	Gln	
				455					460					465	
Ser	Val	Lys	His	His	Arg	Ser	Leu	Ser	Ser	Cys	Cys	Ser	Pro	Gly	
				470					475					480	
Gln	Arg	Ser	Gly	Met	Leu	His	Arg	Asn	Ala	Phe	Arg	Arg	Thr	Pro	
				485					490					495	

Pro	Ser	Pro	Arg	Ser	Arg	Leu	Gly	Gly	Ile	Val	Gly	Pro	Ala	Tyr	500	505	510
Gln	Gln	Leu	Glu	Glu	Ser	Arg	Ile	Pro	Asp	Gln	Asp	Thr	Ile	Pro	515	520	525
Cys	Gln	Gly	Ile	Glu	Val	Arg	Lys	Thr	Ile	Ser	His	Leu	Pro	Ile	530	535	540
Gln	Leu	Trp	Cys	Val	Glu	Arg	Pro	Leu	Asp	Leu	Lys	Tyr	Ser	Ser	545	550	555
Ser	Gly	Leu	Lys	Thr	Gln	Arg	Asn	Thr	Ser	Ile	Asn	Met	Gln	Leu	560	565	570
Pro	Ser	Arg	Glu	Thr	Asn	Pro	Tyr	Phe	Asn	Ser	Leu	Glu	Gln	Lys	575	580	585
Asp	Leu	Val	Gly	Tyr	Ser	Ser	Thr	Arg	Ala	Ser	Ser	Val	Pro	Ile	590	595	600
Ile	Pro	Ser	Val	Gly	Leu	Glu	Glu	Thr	Cys	Leu	Gln	Met	Pro	Gly	605	610	615
Ile	Ser	Glu	Val	Lys	Ser	Ile	Lys	Trp	Cys	Lys	Asn	Ser	Tyr	Ser	620	625	630
Ala	Asp	Val	Val	Asn	Val	Ser	Ile	Pro	Val	Ser	Asp	Cys	Leu	Ile	635	640	645
Ala	Glu	Gln	Gln	Glu	Val	Lys	Ile	Leu	Leu	Glu	Thr	Val	Gln	Glu	650	655	660
Gln	Ile	Arg	Ile	Leu	Thr	Asp	Ala	Arg	Arg	Ser	Glu	Asp	Tyr	Glu	665	670	675
Leu	Ala	Ser	Val	Glu	Thr	Glu	Asp	Ser	Ala	Ser	Glu	Asn	Thr	Ala	680	685	690
Phe	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Lys	Ser	Glu	Arg	Glu	Ala	Gln	695	700	705
Phe	Val	Leu	Arg	Asn	Glu	Ile	Gln	Arg	Asp	Ser	Ala	Leu	Thr	Lys	710	715	720

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3 extracellular domain/Amino AcidSeq
- (B) LOCATION: 1-360
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ser	Glu	Gly	Ala	Ala	Ala	Ala	Ser	Pro	Pro	Gly	Ala	Ala	Ser	
1				5				10						15	
Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	
				20				25						30	
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	
				35				40						45	
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	
				50				55						60	
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	
				65				70						75	
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	
				80				85						90	
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	
				95				100						105	
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	
				110				115						120	
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	
				125				130						135	
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	
				140				145						150	
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	
				155				160						165	
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	
				170				175						180	

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Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	200	205	210
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	245	250	255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr	260	265	270
Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu	275	280	285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn	290	295	300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys	305	310	315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln	320	325	330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His	335	340	345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln	350	355	360

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: NRG3 EGF-like domain/amino acid seq.
- (B) LOCATION: 1-47
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Phe Lys Pro Cys Arg Asp Lys Asp Leu Ala Tyr Cys Leu Asn  
1 5 10 15  
Asp Gly Glu Cys Phe Val Ile Glu Thr Leu Thr Gly Ser His Lys  
20 25 30  
His Cys Arg Cys Lys Glu Gly Tyr Gln Gly Val Arg Cys Asp Gln  
35 40 45  
Phe Leu  
47

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

- (ix) FEATURE:  
(A) NAME/KEY: cARIA.egf  
(B) LOCATION: 1-48  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala Phe Cys Val Asn  
1 5 10 15  
Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn Pro Pro Arg  
20 25 30  
Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln  
35 40 45  
Asn Tyr Val  
48

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

- (ix) FEATURE:  
(A) NAME/KEY: hAR.egf  
(B) LOCATION: 1-45  
(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys Lys Asn Pro Cys Asn Ala Glu Phe Gln Asn Phe Cys Ile His  
1 5 10 15  
Gly Glu Cys Lys Tyr Ile Glu His Leu Glu Ala Val Thr Cys Lys  
20 25 30  
Cys Gln Gln Glu Tyr Phe Gly Glu Arg Cys Gly Glu Lys Ser Met  
35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hBTC.efg
- (B) LOCATION: 1-45
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

His Phe Ser Arg Cys Pro Lys Gln Tyr Lys His Tyr Cys Ile Lys  
1 5 10 15  
Gly Arg Cys Arg Phe Val Val Ala Glu Gln Thr Pro Ser Cys Val  
20 25 30  
Cys Asp Glu Gly Tyr Ile Gly Ala Arg Cys Glu Arg Val Asp Leu  
35 40 45

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hEGF.egf
- (B) LOCATION: 1-46
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His  
1 5 10 15  
Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys  
20 25 30  
Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp  
35 40 45  
Leu  
46

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: hHB-EGF.egf  
(B) LOCATION: 1-45  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Lys Arg Asp Pro Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His  
1 5 10 15  
Gly Glu Cys Lys Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Ile  
20 25 30  
Cys His Pro Gly Tyr His Gly Glu Arg Cys His Gly Leu Ser Leu  
35 40 45

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(ix) FEATURE:

(A) NAME/KEY: hHRGalpha.egf  
(B) LOCATION: 1-49  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15  
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg  
20 25 30  
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr  
35 40 45  
Glu Asn Tyr Pro  
49

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hHRGbeta.egf  
(B) LOCATION: 1-48  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn  
1 5 10 15  
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg  
20 25 30  
Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln  
35 40 45  
Asn Tyr Val  
48

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hTGFalpha.egf  
(B) LOCATION: 1-45  
(C) IDENTIFICATION METHOD:

[illegible]

His 1	Phe	Asn	Asp	Cys 5	Pro	Asp	Ser	His	Thr 10	Gln	Phe	Cys	Phe	His 15
Gly	Thr	Cys	Arg	Phe 20	Leu	Val	Gln	Glu	Asp 25	Lys	Pro	Ala	Cys	Val 30
Cys	His	Ser	Gly	Tyr 35	Val	Gly	Ala	Arg	Cys 40	Glu	His	Ala	Asp	Leu 45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 45 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(A) NAME/KEY: mEPR.egf  
(B) LOCATION: 1-45  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

Gln	Ile	Thr	Lys	Cys	Ser	Ser	Asp	Met	Asp	Gly	Tyr	Cys	Leu	His
1				5					10					15
Gly	Gln	Cys	Ile	Tyr	Leu	Val	Asp	Met	Arg	Glu	Lys	Phe	Cys	Arg
				20					25					30
Cys	Glu	Val	Gly	Tyr	Thr	Gly	Leu	Arg	Cys	Glu	His	Phe	Phe	Leu
				35					40					45

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(A) NAME/KEY: Oligonucleotide probe  
(B) LOCATION: 1-50  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Thr Gly Gly Thr Ala Ala Ala Ala Gly Cys Thr Ala Cys Ala Gly  
1 5 10 15  
Thr Cys Thr Cys Ala Ala Ala Gly Cys Ala Thr Cys Cys Ala Gly  
20 25 30  
Cys Ala Cys Ala Ala Thr Gly Gly Cys Ala Ala Ala Gly Thr Cys  
35 40 45  
Ala Gly Ala Gly Ala  
50

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 transmembrane proximal 1
- (B) LOCATION: 1-8
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asn Asp Gly Glu Cys Phe Val Ile  
1 5 8

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: hNRG3B1 transmembrane proximal 2
- (B) LOCATION: 1-9
- (C) IDENTIFICATION METHOD:
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu Phe Met Glu Ser Glu Glu Val Tyr  
1 5 9

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 466 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: EST Genbank entry H23651  
(B) LOCATION: 1-466  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTTCTGCC GAAAACTGAT TCCATCTTAT CGGATCCAAC AGACCACTTG 50  
GGGATTGAAT TCATGGAGAG TGAAGAAGTT TATCAAAGGC AGGTGCTGTC 100  
AATTTTCATGT ATCATCTTTG GAATTGTCAT CGTGGGCATG TTCTGTGCAG 150  
CATTCTACTT CAAAAGCAAG AAACAAGCTA AACAAATCCA AGAGCAGCTG 200  
AAAGTGCCAC AAAATGGTAA AAGCTACAGT CTCAAAGCAT CCAGCACAAT 250  
GGCAAAGTCA GAGAACTTGG TGAAGAGCCA TGTCCAGCTG CAAAATAAAA 300  
TGTCAGGCTT CTGAGCCCAA GCTAAGCCAT CATATCCCCT GTNGACCTGC 350  
ACGTGCACAT CCNGATGGCC CGTTTCCTGC CTTTTNTGAT GACATTTNCA 400  
CCACAAATGN AGTGAAAATG GGNCTTTTCN TGCCTTAACT GGTGACNTT 450  
TTTNCCCCAA AAGGAG 466

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 2091 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(ix) FEATURE:

- (A) NAME/KEY: Human NRG3B2 (hNRGB2)  
(B) LOCATION: 1-2091  
(C) IDENTIFICATION METHOD:  
(D) OTHER INFORMATION:



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGAGTGAAG GGGCGGCCGC TGCCTCGCCA CCTGGTGCCG CTTCGGCAGC 50  
CGCCGCCTCG GCCGAGGAGG GCACCGCGGC GGCTGCGGCG GCGGCAGCGG 100  
CGGGCGGGGG CCCGGACGGC GGC GGCGAAG GGGCGGCCGA GGGGGGGGG 150  
GAGTTACGCT GTAGCGACTG CATCGTGTGG AACCGGCAGC AGACGTGGCT 200  
GTGCGTGGTA CCTCTGTTCA TCGGCTTCAT CGGCCTGGGG CTCAGCCTCA 250  
TGCTTCTCAA ATGGATCGTG GTGGGCTCCG TCAAGGAGTA CGTGCCCACC 300  
GACCTAGTGG ACTCCAAGGG GATGGGCCAG GACCCCTTCT TCCTCTCAA 350  
GGCCAGCTCT TTCCCAAGG CCATGGAGAC CACCACCACT ACCACTTCCA 400  
CCACGTCCCC CGCCACCCCC TCCGCCGGGG GTGCCGCCTC CTCCAGGACG 450  
CCCAACCGGA TTAGCACTCG CCTGACCACC ATCACGCGGG CGCCCACTCG 500  
CTTCCCCGGG CACCGGGTGC CCATCCGGGC CAGCCCGCGC TCCACCACAG 550  
CACGGAACAC TCGGGCCCCCT GCGACGGTCC CGTCCACCAC GGCCCCGTTC 600  
TTCAGTAGCA GCACGCTGGG CTCCCGACCC CCGGTGCCAG GAACTCCAAG 650  
TACCCAGGCA ATGCCCTCCT GGCCTACTGC GGCATACGCT ACCTCCTCCT 700  
ACCTTCACGA TTCTACTCCC TCCTGGACCC TGTCTCCCTT TCAGGATGCT 750  
GCCTCCTCTT CTTCTCTTTC TTCCTCCTCC GCTACCACCA CCACACCAGA 800  
AACTAGCACC AGCCCCAAAT TTCATACGAC GACATATTCC ACAGAGCGAT 850  
CCGAGCACTT CAAACCCTGC CGAGACAAGG ACCTTGCATA CTGTCTCAAT 900  
GATGGCGAGT GCTTTGTGAT CGAAACCCTG ACCGGATCCC ATAAACACTG 950  
TCGGTGCAAA GAAGGCTACC AAGGAGTCCG TTGTGATCAA TTTCTGCCGA 1000  
AAACTGATTC CATCTTATCG GATCCAACAG ACCACTTGGG GATTGAATTC 1050  
ATGGAGAGTG AAGAAGTTTA TCAAAGGCAG GTGCTGTCAA TTTCATGTAT 1100  
CATCTTTGGA ATTGTCATCG TGGGCATGTT CTGTGCAGCA TTCTACTTCA 1150  
AAAGCAAGAA ACAAGCTAAA CAAATCCAAG AGCAGCTGAA AGTGCCACAA 1200  
AATGGTAAAA GCTACAGTCT CAAAGCATCC AGCACAATGG CAAAGTCAGA 1250

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GAACTTGGTG AAGAGCCATG TCCAGCTGCA AAATTATTCA AAGGTGGAAA 1300  
 GGCATCCTGT GACTGCATTG GAGAAAATGA TGGAGTCAAG TTTTGTCTGGC 1350  
 CCCCAGTCAT TCCCTGAGGT CCCTTCTCCT GACAGAGGAA GCCAGTCTGT 1400  
 CAAACACCAC AGGAGTCTAT CCTCTTGCTG CAGCCCAGGG CAAAGAAGTG 1450  
 GCATGCTCCA TAGGAATGCC TTCAGAAGGA CACCCCCGTC ACCCCGAAGT 1500  
 AGGCTAGGTG GAATTGTGGG ACCAGCATAT CAGCAACTCG AAGAATCAAG 1550  
 GATCCCAGAC CAGGATACGA TACCTTGCCA AGGGTATTCA TCCAGTGGTT 1600  
 TAAAAACCCA ACGAAATACA TCAATAAATA TGCAACTGCC TTCAAGAGAG 1650  
 ACAAACCCCT ATTTTAATAG CTTGGAGCAA AAGGACCTGG TGGGCTATTC 1700  
 ATCCACAAGG GCCAGTTCTG TGCCCATCAT CCCTTCAGTG GGTTTAGAGG 1750  
 AAACCTGCCT GCAAATGCCA GGGATTTCTG AAGTCAAAAG CATCAAATGG 1800  
 TGCAAAACT CCTATTCAGC TGACGTTGTC AATGTGAGTA TTCCAGTCAG 1850  
 CGATTGTCTT ATAGCAGAAC AACAAGAAGT GAAAATATTG CTAGAACTG 1900  
 TCCAGGAGCA GATCCGAATT CTGACTGATG CCAGACGGTC AGAAGACTAC 1950  
 GAACTGGCCA GCGTAGAAAC CGAGGACAGT GCAAGTGAAA ACACAGCCTT 2000  
 TCTCCCCCTG AGTCCCACAG CCAAATCAGA ACGAGAGGCG CAATTTGTCT 2050  
 TAAGAAATGA AATACAAAGA GACTCTGCAT TGACCAAGTG A 2091

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 696 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

- (ix) FEATURE:
  - (A) NAME/KEY: Human NRG3B2
  - (B) LOCATION: 1-696
  - (C) IDENTIFICATION METHOD:
  - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Ser Glu Gly Ala Ala Ala Ala Ser Pro Pro Gly Ala Ala Ser  
 1 5 10 15

Ala	Ala	Ala	Ala	Ser	Ala	Glu	Glu	Gly	Thr	Ala	Ala	Ala	Ala	Ala	20	25	30
Ala	Ala	Ala	Ala	Gly	Gly	Gly	Pro	Asp	Gly	Gly	Gly	Glu	Gly	Ala	35	40	45
Ala	Glu	Pro	Pro	Arg	Glu	Leu	Arg	Cys	Ser	Asp	Cys	Ile	Val	Trp	50	55	60
Asn	Arg	Gln	Gln	Thr	Trp	Leu	Cys	Val	Val	Pro	Leu	Phe	Ile	Gly	65	70	75
Phe	Ile	Gly	Leu	Gly	Leu	Ser	Leu	Met	Leu	Leu	Lys	Trp	Ile	Val	80	85	90
Val	Gly	Ser	Val	Lys	Glu	Tyr	Val	Pro	Thr	Asp	Leu	Val	Asp	Ser	95	100	105
Lys	Gly	Met	Gly	Gln	Asp	Pro	Phe	Phe	Leu	Ser	Lys	Pro	Ser	Ser	110	115	120
Phe	Pro	Lys	Ala	Met	Glu	Thr	Thr	Thr	Thr	Thr	Thr	Ser	Thr	Thr	125	130	135
Ser	Pro	Ala	Thr	Pro	Ser	Ala	Gly	Gly	Ala	Ala	Ser	Ser	Arg	Thr	140	145	150
Pro	Asn	Arg	Ile	Ser	Thr	Arg	Leu	Thr	Thr	Ile	Thr	Arg	Ala	Pro	155	160	165
Thr	Arg	Phe	Pro	Gly	His	Arg	Val	Pro	Ile	Arg	Ala	Ser	Pro	Arg	170	175	180
Ser	Thr	Thr	Ala	Arg	Asn	Thr	Ala	Ala	Pro	Ala	Thr	Val	Pro	Ser	185	190	195
Thr	Thr	Ala	Pro	Phe	Phe	Ser	Ser	Ser	Thr	Leu	Gly	Ser	Arg	Pro	200	205	210
Pro	Val	Pro	Gly	Thr	Pro	Ser	Thr	Gln	Ala	Met	Pro	Ser	Trp	Pro	215	220	225
Thr	Ala	Ala	Tyr	Ala	Thr	Ser	Ser	Tyr	Leu	His	Asp	Ser	Thr	Pro	230	235	240
Ser	Trp	Thr	Leu	Ser	Pro	Phe	Gln	Asp	Ala	Ala	Ser	Ser	Ser	Ser	245	250	255
Ser	Ser	Ser	Ser	Ser	Ala	Thr	Thr	Thr	Thr	Pro	Glu	Thr	Ser	Thr	260	265	270

Ser	Pro	Lys	Phe	His	Thr	Thr	Thr	Tyr	Ser	Thr	Glu	Arg	Ser	Glu
				275					280					285
His	Phe	Lys	Pro	Cys	Arg	Asp	Lys	Asp	Leu	Ala	Tyr	Cys	Leu	Asn
				290					295					300
Asp	Gly	Glu	Cys	Phe	Val	Ile	Glu	Thr	Leu	Thr	Gly	Ser	His	Lys
				305					310					315
His	Cys	Arg	Cys	Lys	Glu	Gly	Tyr	Gln	Gly	Val	Arg	Cys	Asp	Gln
				320					325					330
Phe	Leu	Pro	Lys	Thr	Asp	Ser	Ile	Leu	Ser	Asp	Pro	Thr	Asp	His
				335					340					345
Leu	Gly	Ile	Glu	Phe	Met	Glu	Ser	Glu	Glu	Val	Tyr	Gln	Arg	Gln
				350					355					360
Val	Leu	Ser	Ile	Ser	Cys	Ile	Ile	Phe	Gly	Ile	Val	Ile	Val	Gly
				365					370					375
Met	Phe	Cys	Ala	Ala	Phe	Tyr	Phe	Lys	Ser	Lys	Lys	Gln	Ala	Lys
				380					385					390
Gln	Ile	Gln	Glu	Gln	Leu	Lys	Val	Pro	Gln	Asn	Gly	Lys	Ser	Tyr
				395					400					405
Ser	Leu	Lys	Ala	Ser	Ser	Thr	Met	Ala	Lys	Ser	Glu	Asn	Leu	Val
				410					415					420
Lys	Ser	His	Val	Gln	Leu	Gln	Asn	Tyr	Ser	Lys	Val	Glu	Arg	His
				425					430					435
Pro	Val	Thr	Ala	Leu	Glu	Lys	Met	Met	Glu	Ser	Ser	Phe	Val	Gly
				440					445					450
Pro	Gln	Ser	Phe	Pro	Glu	Val	Pro	Ser	Pro	Asp	Arg	Gly	Ser	Gln
				455					460					465
Ser	Val	Lys	His	His	Arg	Ser	Leu	Ser	Ser	Cys	Cys	Ser	Pro	Gly
				470					475					480
Gln	Arg	Ser	Gly	Met	Leu	His	Arg	Asn	Ala	Phe	Arg	Arg	Thr	Pro
				485					490					495
Pro	Ser	Pro	Arg	Ser	Arg	Leu	Gly	Gly	Ile	Val	Gly	Pro	Ala	Tyr
				500					505					510
Gln	Gln	Leu	Glu	Glu	Ser	Arg	Ile	Pro	Asp	Gln	Asp	Thr	Ile	Pro
				515					520					525

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Cys	Gln	Gly	Tyr	Ser	Ser	Ser	Gly	Leu	Lys	Thr	Gln	Arg	Asn	Thr
				530					535					540
Ser	Ile	Asn	Met	Gln	Leu	Pro	Ser	Arg	Glu	Thr	Asn	Pro	Tyr	Phe
				545					550					555
Asn	Ser	Leu	Glu	Gln	Lys	Asp	Leu	Val	Gly	Tyr	Ser	Ser	Thr	Arg
				560					565					570
Ala	Ser	Ser	Val	Pro	Ile	Ile	Pro	Ser	Val	Gly	Leu	Glu	Glu	Thr
				575					580					585
Cys	Leu	Gln	Met	Pro	Gly	Ile	Ser	Glu	Val	Lys	Ser	Ile	Lys	Trp
				590					595					600
Cys	Lys	Asn	Ser	Tyr	Ser	Ala	Asp	Val	Val	Asn	Val	Ser	Ile	Pro
				605					610					615
Val	Ser	Asp	Cys	Leu	Ile	Ala	Glu	Gln	Gln	Glu	Val	Lys	Ile	Leu
				620					625					630
Leu	Glu	Thr	Val	Gln	Glu	Gln	Ile	Arg	Ile	Leu	Thr	Asp	Ala	Arg
				635					640					645
Arg	Ser	Glu	Asp	Tyr	Glu	Leu	Ala	Ser	Val	Glu	Thr	Glu	Asp	Ser
				650					655					660
Ala	Ser	Glu	Asn	Thr	Ala	Phe	Leu	Pro	Leu	Ser	Pro	Thr	Ala	Lys
				665					670					675
Ser	Glu	Arg	Glu	Ala	Gln	Phe	Val	Leu	Arg	Asn	Glu	Ile	Gln	Arg
				680					685					690
Asp	Ser	Ala	Leu	Thr	Lys									
				695	696									

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